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SEQ ID NO:1

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B.

SEQ ID NO:2

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Fig. 1

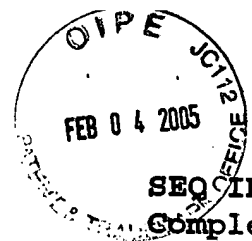


Figure 2A

SEQ ID NO : 3

Complete genome sequence of bacteriophage 77

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Figure 2B

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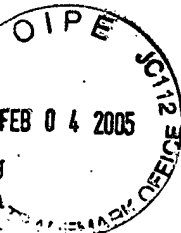


Figure 2C

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Figure 2D

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Figure 2E

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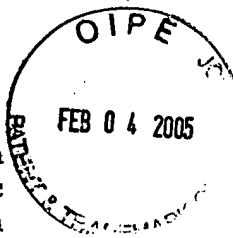


Figure 2F

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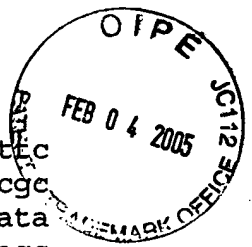


Figure 2G

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Figure 2H

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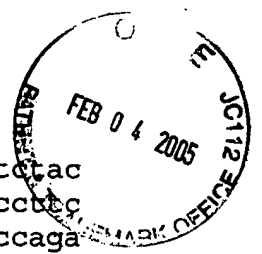


Figure 2I

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Figure 2J

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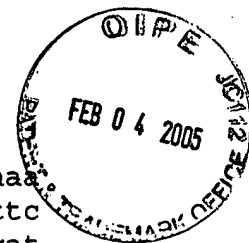


Figure 2K

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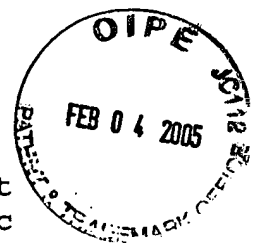


Figure 2L

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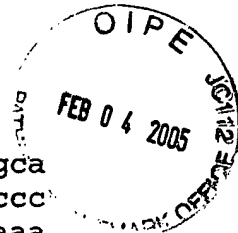
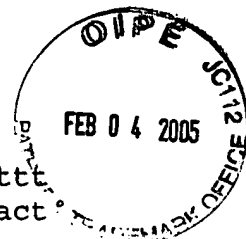


Figure 2M

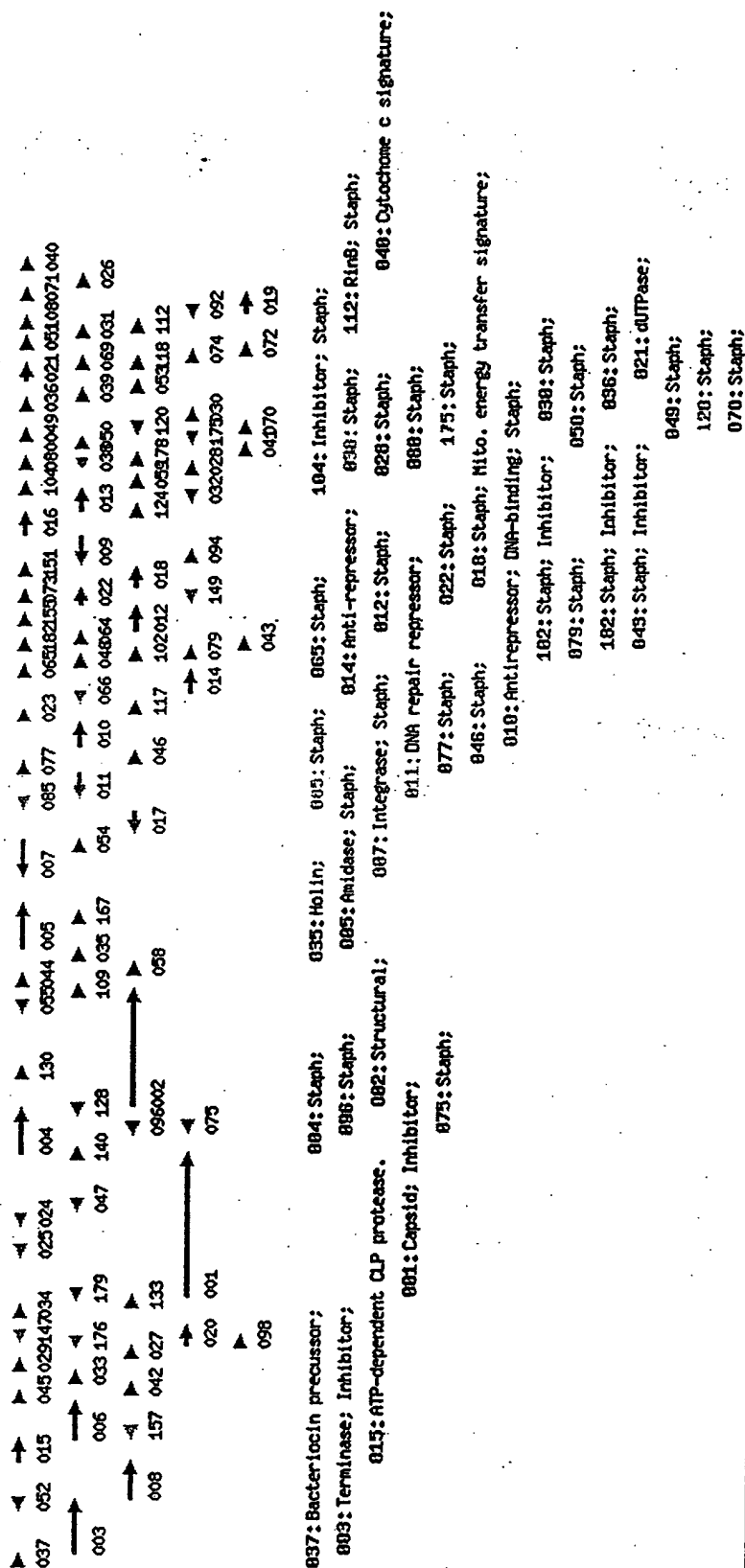
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36961	tgatttcaac	aggttataaa	agtttcaatg	aagtaaaact	attacaatac	acaggattta
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37081	aagtaagttt	tatcgagttt	aaagaaggag	cctttttatat	aacttttagc	aatgtaactg
37141	aattactaag	tgaaaatgac	gatattattg	aaattgttgg	aaatattttt	gaaaatgaga
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37321	caagaagcaa	cgagatgagc	ttattgggga	tatagcgaag	ttacgagatt	gtaacaaaga
37381	tctagagaag	aaagcaagcg	catgggatag	gtattgcaag	agcgttgaaa	aagatttaat
37441	aaacgaattc	ggtaacgatg	atgaaagagt	taaattcgga	atggaattaa	acaataaaat
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38101	gatggattaa	taagcatttt	agatataaaa	ggtaactatg	tacaagatgg	aagaggcata
38161	agaagagttt	accaaataca	caaaggcgat	aaactagctc	aattgggttat	cgtgcctata
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38281	ggcttcggaa	gtagcggagt	gtaaagacat	cttagatcga	gttaaggagg	ttttggggaa
38341	gtgacgcaat	acttagtcac	aacattcaaa	gattcaacag	gacgaccaca	tgaacatatt
38401	actgtggcta	gagataatca	gacgtttaca	gttattgagg	cagagagtaa	agaagaagcg
38461	aaagagaagt	acgaggcaca	agttaaaaga	gatgcagtta	ttaaagtggg	tcagttgtat
38521	gaaaatataa	gggagtgtgg	gaaatgacgg	atgttaaaat	taaaactatt	tcaggtggag
38581	tttattttgt	aaaaacagct	gaaccttttg	aaaaatatgt	tgaaagaatg	acgagtttta
38641	atgggttatat	ttacgcaagt	actataatca	agaaaccaac	gtatattaaa	acagatacga
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Figure 2N

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38881 tgtattgaac aaagggtata tagttgggat caatgthgag gaggcagatg atgattaaca
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39001 cacctgaaga aaaggctaag attgaagatg atthttattaa agaaattaaa gataaagaca
39061 gtgaattthta cagtcctacg atggctaata tgaatgaata tgaattaagg gctatgthta
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39181 atggatgggt tgcacatctt tattgthtga atactgtcat tattcggtat attcgcatg
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39301 caaggaacta ttacagataa atataacaag agacaagata aagaagacaa gthctatatt
39361 gtattagaca acaacaagt cattgaaaat tccgacttat tattcaaaaa gaaatttgat
39421 agcgcagata tacaagctag gthaaaagta ggcgataagg tagaagthta aacaatcggt
39481 tatagaatac actthtttaa tttatatccg gthcttatacg aagthaaagaa ggtagataaa
39541 caatgattaa acaataacta agactattat tcttactagc aatgtatgag ttaggthaagt
39601 atgthaactga gcaagtgtat attatgatga cggctaata tgaatgtagag gcgccgagtg
39661 attacgtctt tgcagcggag gtgagthaat aatgagaata thttatthtattg atttgatcgt
39721 thtgctgtht gctthtcttaa tatccatata tattattgat gatggagthg taataaatgc
39781 attaggaatt thtggtatgt ataaaattat agatthcttht tcagaaaaata ttataaagag
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39901 gctthattca gthaaagaga thttthaggta thttacagat tctaacttac aacgtaaaaa
39961 aatcaattta gaacaaatat atccgatata thtagattgt thtaaaaaagg ctaaaaaagat
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40081 agthctthaat aattthagata agcaaagthaa aaaagcgtat gaaatgthta thggattthg
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40261 tattataaat gaatatcaaa aagatatatc thtattthaaa aatataatta ataaaatgaa
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40981 gatgaggata cgctthgagtht attaaggtht agatattggg attgtctctat tggthgtht
41041 gaatgggaag atatagcaca thactthtggg acaagthaga caagtatatt acgtagaagg
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41161 tghaagthccg cattaaaaca gththattatg thtagthtcatg attaatattt aaagthatta
41221 aatgctaata cgacgcataa acaagaggcg catcactatg tgatgtgtct thttatttht
41281 gaggtatgaa catgthtcaa ctaattgthaa atacattact acacatcaag tatagatgag
41341 tctthgatact actthaagtht tataaggthg aacattatga tgactaaaga cgaacgtata
41401 cgattctata agthctaaaga atggcaaata acaagaaaaa gagtgtctaga aagagataat
41461 tatgaatgth aacaatgthaa gagagacggc aagthtaacga catatgacaa aagcaagcgt
41521 aagthcgtthg atgtagatca tatattatcg ctagaacatc atccggagtht tgcctcatgac
41581 thaaacaatt tagaaacact gthgattthaa tgtcacacaa aaaaagaaaa gagattthata
41641 aaaaaagaaa ataaatggaa agacgaaaaa tggthaaatac ccccggtca aaaaaatcaa
41701 aagcagthc



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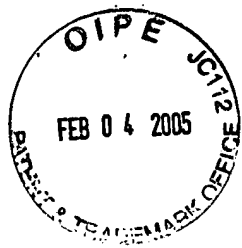


Fig. 4

P77ORF104

SEQ ID NO: 4

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61  ctcatagatg aggcacaggg cgatgaaaat aggttgtagc acctatttat ccaaaaactt
121 gcagaacgtc atacacgccc cgctatcgtc gaatattaa
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SEQ ID NO: 5

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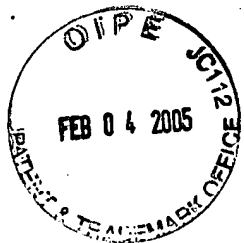


Fig. 5

Predicted Tryptic Peptide Masses of Conceptual ORF in Contig 1383:

```
1  M G G G Q S I M K q f k S I I N T S Q D F E K r I E K j k K 30
31  e v i n d p d v k Q F L E A H R a e l t n a m i d e d i n v 60
61  l q e y k D Q Q K h y d g h k F A D C P N F V K g h v p e l 90
91  y v d n n r I K i r Y L Q C P C K i k Y D E E R t e a e l i 120
121 t s h n m q r D T L N A K i k D I Y M N H R d r L D V A M A 150
151 A D D I C T A I T N G E Q V K g l y l y g p f g t g k S F I 180
181 L G A I A N Q L K s k K v r S T I I Y L P E F I R t i k G G 210
211 F K d g s f e k K i h r V R e a n i m i d d i g a e e v t 240
241 p w v r D E V I G P L L H Y R m v h e l p t f f s s n f d y 270
271 s e l e h h l a m t r D G E E K t k A A R i e r V K s l s 300
301 t p y f l s g e n f r N N 313
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Tryptic peptide fragment:

GHVPELYVDNNR

Predicted Peptide Mass MH+ = 1413.538

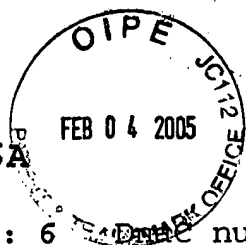
STIIYLPEFIR

Predicted Peptide Mass MH+ = 1352.6221

SLSTPYFLSGENFR

Predicted Peptide Mass MH+ = 1618.7923

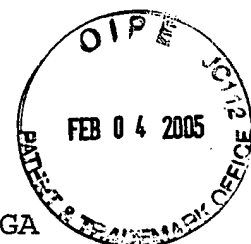
Figure 6A



SEQ ID NO: 6 nucleotide *B. subtilis*

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1   ATGACAGACC TTCTGAATGA CCGGCTTCCT CCGCAAAATA TAGAAGCCGA
51  ACAAGCCGTG TTAGGCGCTA TTTTTTTACA GCCGTCTGCT TTAACACTGG
101 C TTCAGAAAGT ATTGATTCCA GATGATTCTT ATAGAATGTC CCACCAAAAA
151 ATCTATAATG CGATGCTGGT GCTCGGTGAC CGAGGTGAAC CGGTTGATCT
201 GGTGACAGTT ACATCAGAGC TTGCGAACAC AGACCTGCTG GAAGAAGTAG
251 GCGGTATTTT ATATTTGACA GATATCGCAA ACTCGGTGCC GACAGCGGCT
301 AACATAGAAT ATTACGCGAA AATCGTTGAG GAAAAATCGA TTCTTCGCCG
351 ATTAATCAGA ACTGCGACAA CGATTGCTCA AGACGGGTAT ACCCGTGAGG
401 ATGAGGTCGA GGATTTACTC AGTGAAGCGG AAAAAACGAT TATGGAAGTG
451 GCACAGCGCA AAAACACGAG TGCCTTCCAA AATATTAAGG ACGTCCTTGT
501 CCAGACCTAT GATAATATCG AACAGCTTTA CAATCGAAAA GGTGATATCA
551 CGGGAATTCC AACAGGGTTT ACGGAGCTTG ACCGGATGAC TGCGGGTTTC
601 CAGCGCAACG ACTTGATCAT TGTGGCTGCC CGTCCTTCAG TAGGGAAAAC
651 AGCCTTTGCC CTGAACATCG CACAAAACGT GCGGACGAAG ACCGATGAGA
701 GCGTAGCGAT TTTCAGTCTT GAGATGGGTG CCGAGCAGCT CGTTATGCGT
751 ATGCTCTGTG CCGAGGGAAA TATCAATGCC CAGAATCTCC GTACAGGTAA
801 CCTGACCGAA GAGGATTGGG GCAAGCTGAC GATGGCAATG GGAAGCCTAT
851 CGAACAGCGG GATTTACATC GATGATACAC CGGGTATTTC AGTGAGTGAA
901 ATCCGTGCCA AGTGCCGCGG CTTGAAGCAG GAAAGCGGGC TGGGCATGAT
951 TTTGATCGAT TACCTGCAAT TGATTCAGGG AAGCGGTCGT TCAAAGGACA
1001 ACCGTCAGCA GGAAGTATCT GAAATTTCCC GTGAACTGAA GTCGATTGCG
1051 AGGGAGCTGC AAGTCCCTGT TATCGCGCTT TCTCAGCTTT CCAGGGGTGT
1101 TGAGCAGCGT CAGGATAAAC GTCCGATGAT GTCTGATATC CGGGAATCAG
1151 GAAGTATCGA GCAGGACGCG GATATTGTCG CGTTCCTTTA TCGTGATGAC
1201 TACTATGACA AAGAAACCGA GAATAAAAAT ATTATCGAAA TTATTATCGC
1251 CAAACAGCGT AACGGCCCGG TAGGAACCGT GTCTCTTGCG TTCGTAAAAG
1301 AATACAACAA ATTCGTCAAC CTGGAACGGC GTTTTGATGA CGCAGGCGTT
1351 CCGCCCGGCG CA
```

Figure 6B



SEQ ID NO: 7 DnaC nucleotide *S. aureus*

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1  ATGGATAGAA TGTATGAGCA AAATCAAATG CCGCATAACA ATGAAGCTGA
51 ACAGTCTGTC TTAGGTTCAA TTATTATAGA TCCAGAATTG ATTAATACTA
101 CTCAGGAAGT TTTGCTTCCT GAGTCGTTTT ATAGGGGTGC CCATCAACAT
151 ATTTTCCGTG CAATGATGCA CTTAAATGAA GATAATAAAG AAATTGATGT
201 TGTAACATTG ATGGATCAAT TATCGACGGA AGGTACGTTG AATGAAGCGG
251 GTGGCCCGCA ATATCTTGCA GAGTTATCTA CAAATGTACC AACGACGCGA
301 AATGTTTCAGT ATTATACTGA TATCGTTTCT AAGCATGCAT TAAAACGTAG
351 ATTGATTCAA ACTGCAGATA GTATTGCCAA TGATGGATAT AATGATGAAC
401 TTGAACTAGA TGCGATTTTA AGTGATGCAG AACGTCGAAT TTTAGAGCTA
451 TCATCTTCTC GTGAAAGCGA TGGCTTTAAA GACATTCGAG ACGTCTTAGG
501 ACAAGTGTAT GAAACAGCTG AAGAGCTTGA TCAAAATAGT GGTCAAACAC
551 CAGGTATACC TACAGGATAT CGAGATTTAG ACCAAATGAC AGCAGGGTTC
601 AACCAGAAATG ATTTAATTAT CCTTGCAGCG CGTCCATCTG TAGGTAAGAC
651 TCGTTCGCA CTTAATATTG CACAAAAGT TGCAACGCAT GAAGATATGT
701 ATACAGTTGG TATTTTCTCG CTAGAGATGG GTGCTGATCA GTTAGCCACA
751 CGTATGATTT GTAGTTCTGG AAATGTTGAC TCAAACCGCT TAAGAACGGG
801 TACTATGACT GAGGAAGATT GGAGTCGTTT TACTATAGCG GTAGGTAAAT
851 TATCACGTAC GAAGATTTTT ATTGATGATA CACCGGGTAT TCGAATTAAT
901 GATTTACGTT CTAAATGTCG TCGATTAAAG CAAGAACATG GCTTAGACAT
951 GATTGTGATT GACTACTTAC AGTTGATTCA AGGTAGTGGT TCACGTGCGT
1001 CCGATAACAG ACAACAGGAA GTTTCTGAAA TCTCTCGTAC ATTAAAAGCA
1051 TTAGCCCGTG AATTAGAATG TCCAGTTATC GCATTAAGTC AGTTATCTCG
1101 TGGTGTTGAA CAACGACAAG ATAAACGTCC AATGATGAGT GATATTCGTG
1151 AATCTGGTTC GATTGAGCAA GATGCCGATA TCGTTGCATT CTTATACCGT
1201 GATGATTACT ATAACCGTGG CGGCGATGAA GATGATGACG ATGATGGTGG
1251 TTTCGAGCCA CAAACGAATG ATGAAAACGG TGAAATTGAA ATTATCATTG
1301 CTAAGCAACG TAACGGTCCA ACAGGCACAG TTAAGTTACA TTTTATGAAA
1351 CAATATAATA AATTTACCGA TATCGATTAT GCACATGCAG ATATGATGTA
1401 A
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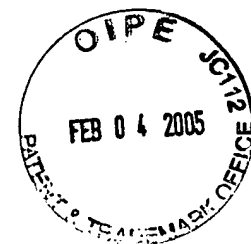


Figure 6C

Optimal global alignment

Sequence 1 SEQ ID NO: 6 DnaC nucleotide *B. subtilis*(1471 letters)

Sequence 2 SEQ ID NO: 7 DnaC nucleotide *S. aureus*(1513 letters)

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seq1 1 AT-GACAGACCTTCTGAATGACCGGCTTC---CTCCGCAAAATATAGAAGCCGAACAAGC 56
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seq2 1 ATGGATAGA---ATGTATGAGCAAAATCAAATGCCGCATAACAATGAAGCTGAACAGTC 56

seq1 57 CGTGTTAGGCGCTATTTTTTTTACAGCC-GTCTGCTTTAACACTGGCTTCAGAAGTATTGA 115
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
seq2 57 TGTCTTAGGTTCAATTATTATAGATCCAGAATTGATTAATACT-ACTCAGGAAGTTTTCG 115

seq1 116 TTCCAGATGATTTCTATAGAATGTCCACCAAAAAATCTATAATGCGATGCTGGTGCTCG 175
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
seq2 116 TTCCTGAGTCGTTTTATAGGGGTGCCCATCAACATATTTTCCGTGCAATGATGCACCTAA 175

seq1 176 GTGACCGAGGTGAACCGGTTGATCTGGTGACA--GTTACATCAGAGCTTGCGAACACAGA 233
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
seq2 176 ATGAAGATAATAAAGAAATTGATGTTGTAACATTGATGGATC--AATTATCGACGGAAGG 233

seq1 234 CCTGCTGGAAGAAGTAGGCGGTATTTTCATAT-TTG-ACAGATATCGCAAACCTCGGTGCCG 291
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
seq2 234 TACGTTGAATGAAGCGGTGGCCCGCAATATCTTGACAGATTATCTACAAAT--GTACCA 291

seq1 292 ACAGCGGCTAACATAGAAATATTACGCGAAAATCGTTGAGGAAAAATCGATT-CTTCGCCC 350
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
seq2 292 ACGACGCGAAATGTTTCAGTATTATACTGATATCGTT-TCTAAGCATGCATTAAAACGTAG 350

seq1 351 ATTAATCAGAACTGCGACAACGATTGCTCAAGACGGGTATACCCGTGAGGATGAGGTCTGA 410
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seq2 351 ATTGATTCAAACCTGCAGATAGTATTGCCAATGATGGATATAATGATGAACCTGAACTAGA 410

seq1 411 --GGATTTACTCAGTGAAGCGGAAAAAACGATTATGGAAGTGGCA-CAGCGCAAAAACAC 467
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
seq2 411 TGCGATTT--TAAGTGATGCAGAACGTCGAATTTTAGAGCTATCATCTTCTCGTGAAAGC 468

seq1 468 GAGTGCCTTCCAAAATATTAAGGACGTCCTTGTCAGACCTATGATAATATC-GAACAGC 526
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
seq2 469 GA-TGGCTTTAAAGACATTCGAGACGTCCTTAGGACAAGTGTATGA-AACAGCTGAAGAGC 526

seq1 527 TTTACAATCGAAAAAGGTGAT--ATCA-CGGGAATTCCAACAGGGTTTACGGAGCTTGACC 583
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
seq2 527 TT--GATCAAAATAGTGGTCAAAACACCAGGTATACCTACAGGATATCGAGATTTAGACC 583

seq1 584 GGATGACTGCGGGTTTCCAGCGCAACGACTTGATCATTTGTGGCTGCCCGTCCTTCAGTAG 643
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seq2 584 AAATGACAGCAGGGTTCAACCGAAATGATTTAATTATCCTTGACGCGCGTCCATCTGTAG 643

seq1 644 GGAAAACAGCCTTTGCCCTGAACATCGCACAAAACGTGGCGAC----GAAGACCGATG-A 698
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
seq2 644 GTAAGACTGCGTTTCGCACTTAATATTGCACAAAAGTTGCAACGCATGAAGA--TATGTA 701
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seq1	699	GAGCGTAGCGATTTTTCAGTCTTGAGATGGGTGCCGAGCAGCTCGTTATGCGTATGCTCTG	
seq2	702	TACAGTTGGTATTTTCTCGCTAGAGATGGGTGCTGATCAGTTAGCCACACGTATGATTTG	761
seq1	759	TGCCGAGGGAAATATCAATGCCCAGAATC---TCCGTACAGGTAACCTGACCGAAGAGGA	815
seq2	762	TAGTTCTGGAAATGT---TGA CTCAAACCGCTTAAGAACGGGTACTATGACTGAGGAAGA	818
seq1	816	TTGGGGCAAGCTGACGATGGCAATGGGAAGCCTATCGAACAGCGGGATTTACATCGATGA	875
seq2	819	TTGGAGTCGTTTTTACTATAGCGGTAGGTAAATTATCACGTACGAAGATTTTTTATTGATGA	878
seq1	876	TACACCGGGTATTTCGAGTGAGTGAAATCCGTGCCAAGTGCCGCCGCTTGAAGCAGGAAAG	935
seq2	879	TACACCGGGTATTTCGAATTAATGATTTACGTTCTAAATGTCGTCGATTAAAGCAAGAACA	938
seq1	936	CGGGCTGGGCATGATTTTGATCGATTACCTGCAATTGATTACAGGGAAGCGGT---CGTTC	992
seq2	939	TGGCTTAGACATGATTGTGATTGACTACTTACAGTTGATTCAAGGTAGTGGTTCACGTGC	998
seq1	993	AAAGGACAACCGTCAGCAGGAAGTATCTGAAATTTCCCGTGAAC TGAAGTCGATTGCGAG	1052
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seq2	1119	AGATAAACGTCCAATGATGAGTGATATTCTGTGAATCTGGTTCGATTGAGCAAGATGCCGA	1178
seq1	1173	TATTGTCGCGTTCCTTTATCGTGATGACTACT-----ATGA	1208
seq2	1179	TATCGTTGCATTCTTATACCGTGATGATTACTATAACCGTGGCGGCGATGAAGATGATGA	1238
seq1	1209	CAAAGA-----AACCGA--GAATAAAA--ATATTATCGAAATTATTAT	1247
seq2	1239	CGATGATGGTGGTFTTCGAGCCACAAACGAATGATGAAAACGGTGAAATTGAAATTATCAT	1298
seq1	1248	CGCCAAACAGCGTAACGGCCCGGTAGGAACCGTGCTCTTGC-GTTCGTAAAAGAATACA	1306
seq2	1299	TGCTAAGCAACGTAAACGGTCCAACAGGCACAGT-TAAGTTACATTTTATGAAACAATATA	1357
seq1	1307	ACAAATTTCGTCAACCTGGAACGGCGTTTTTGATGACGCAGGCGTTCGCCCGGCGCA	1362
seq2	1358	ATAAATT---TACCGATATCG--ATTATGCACATGCAGATATGATG-----TAA	1401

FEB 04 2005

Figure 6D

SEQ ID NO: 8 DnaC *B. subtilis*

```

1   MTDLLNDRLP PQNIEAEQAV LGAIFLQPSA LTLASEVLIP DDFYRMSHQK
51  IYNAMLVLGD RGEVVDLVTV TSELANTDLL EEVGGISYLT DIANSVPTAA
101 NIEYYAKIVE EKSILRRLIR TATTIAQDGY TREDEVEDLL SEAEKTIMEV
151 AQRKNTSAFQ NIKDVLVQTY DNIEQLYNRK GDITGIPTGF TELDRMTAGF
201 QRNDLIIVAA RPSVGKTAFV LNIAQNVATK TDESVAIFSL EMGAEQLVMR
251 MLCAEGNINA QNLRTGNLTE EDWGKLTAM GSLSNSGIYI DDTPGIRVSE
301 IRAKCRRLKQ ESGGLMILID YLQLIQGSGR SKDNRQQEVS EISRELKSIA
351 RELQVPVIAL SQLSRGVEQR QDKRPMMSDI RESGSIEQDA DIVAFLYRDD
401 YYDKETENKN IIEIIIAKQR NGPVGTVSLA FVKEYNKFVN LERRFDDAGV
451 PPGA

```

SEQ ID NO: 9 DnaC *S. aureus*

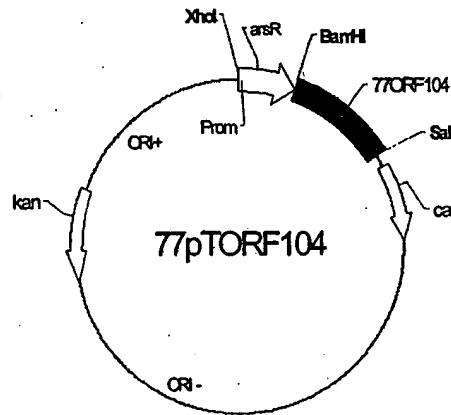
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1   MDRMYEQNQV PHNNEAEQSV LGSIIIDPEL INTTQEVLLP ESFYRGAHQH
51  IFRAMMHLNE DNKEIDVVTI MDQLSTEGTL NEAGGPQYLA ELSTNVPTTR
101 NVQYYTDIVS KHALKRRLIQ TADSIANDGY NDELELDAIL SDAERRILEL
151 SSSRES DGFK DIRDVLGQVY ETAEELDQNS GQTPGIPTGY RDLDQMTAGF
201 NRNDLIILAA RPSVGKTAFV LNIAQKVATH EDMYTVGIFS LEMGADQLAT
251 RMICSSGNVD SNRLRTGTMT EEDWSRFTIA VGKLSRTKIF IDDTPGIRIN
301 DLRSKCRRLK QEHGLDMIVI DYQLIQGSG SRASDNRQQE VSEISRTLKA
351 LARELECPVI ALSQLSRGVE QRQDKRPMMS DIRESGSIEQ DADIVAFLYR
401 DDYYNRGGDE DDDDDGGFEP QTNDENGEIE IIIAKQRNGP TGTVKLHFMK
451 QYNKFTDIDY AHADMM

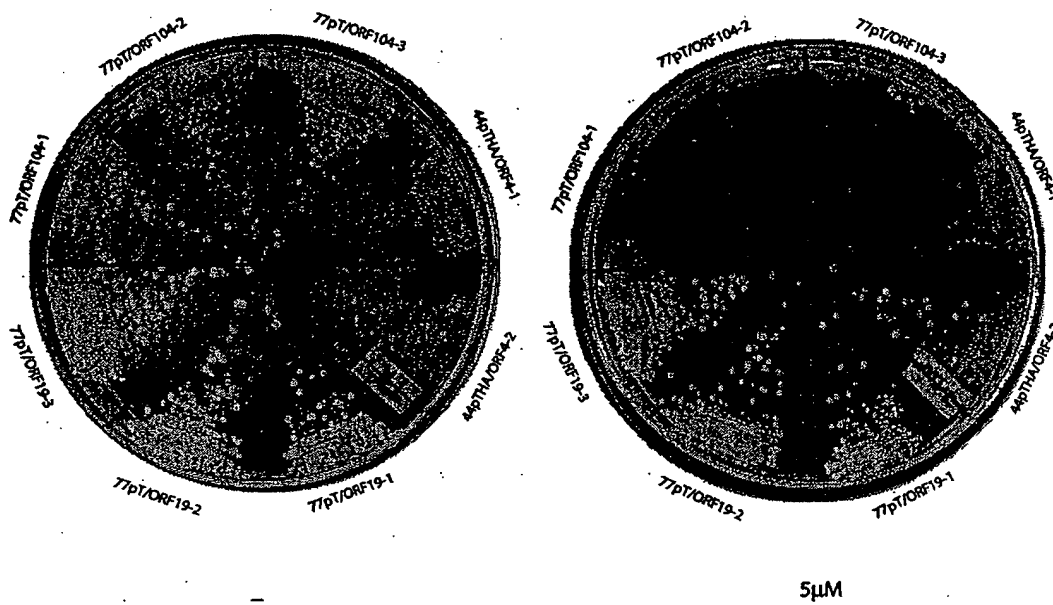
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FIGURE 7

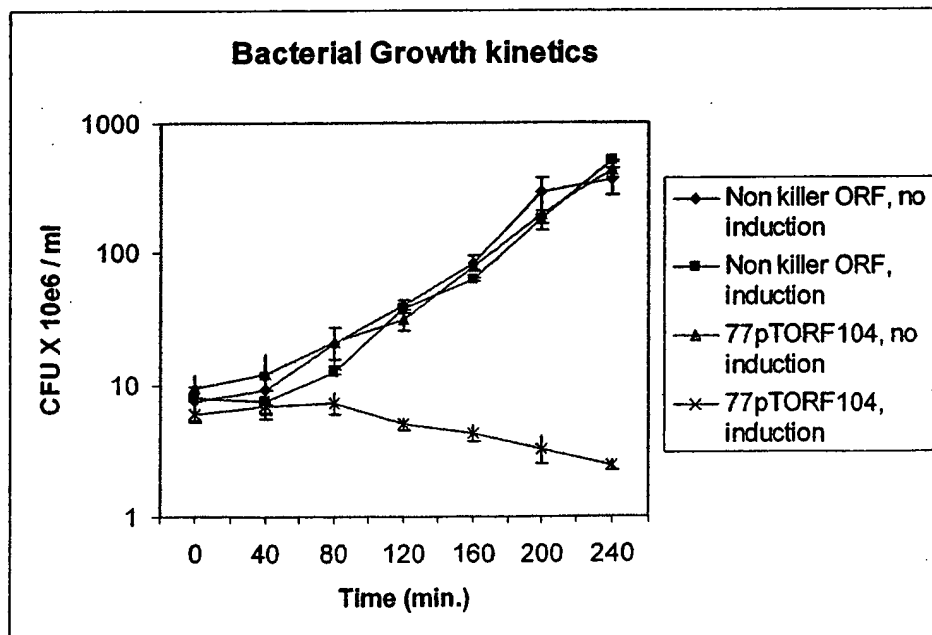
7A-



7B-



7C-





GST

GST/ORF104

ACB 0 0.1 0.5 1.0 2.0 ACB 0 0.1 0.5 1.0 2.0 Mr

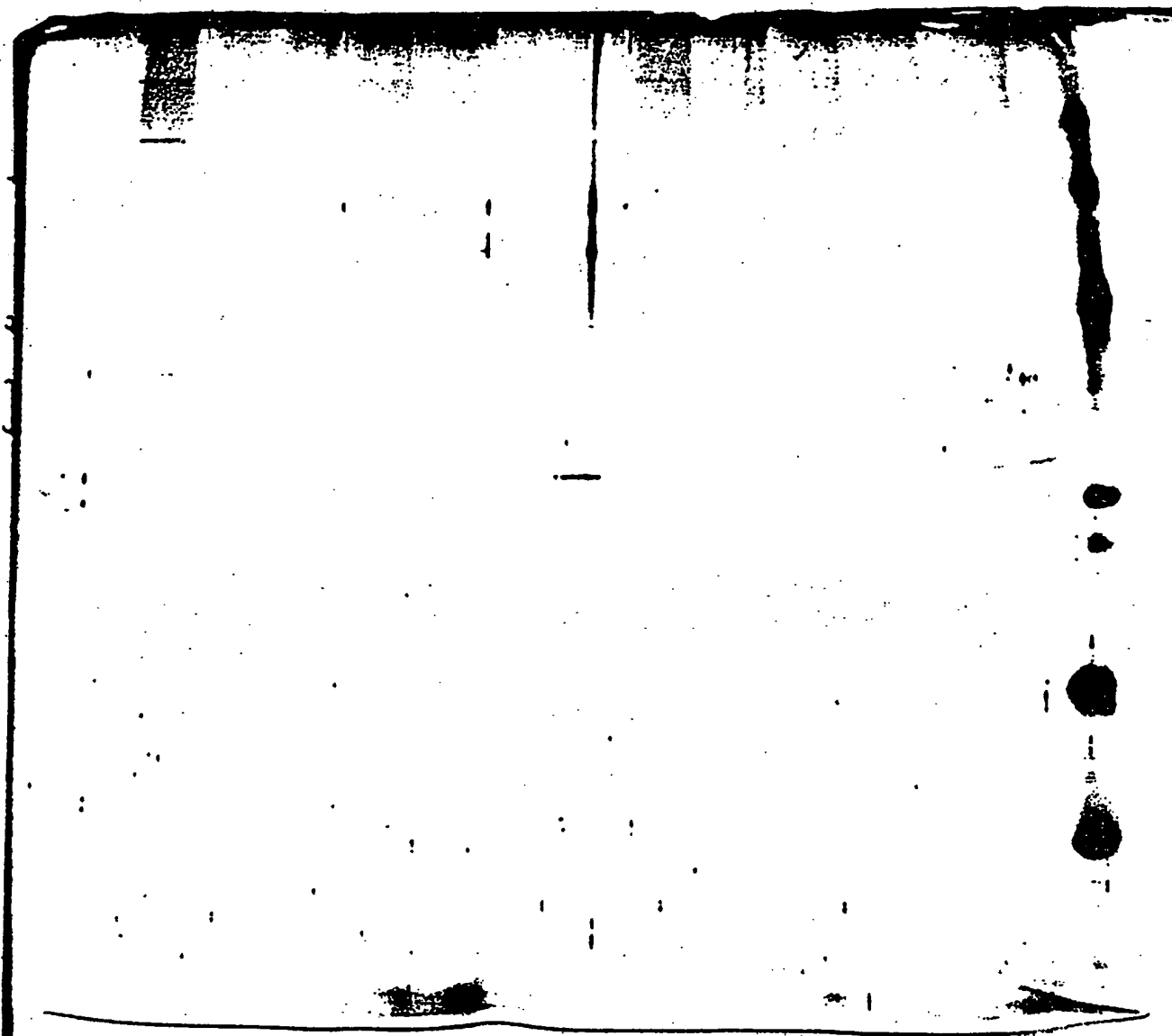
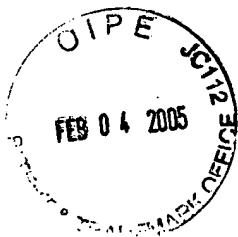


Fig. 8 A



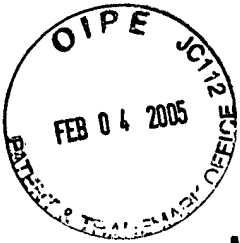
GST

GST/ORF104

ACB 0 0.1 0.5 1.0 2.0 Mr

ACB 0 0.1 0.5 1.0 2.0

83



GST

GST/ ORF104

Mr ACB 0 0.1 0.5 1.0 2.0 ACB 0 0.1 0.5 1.0 2.0

97

66

45

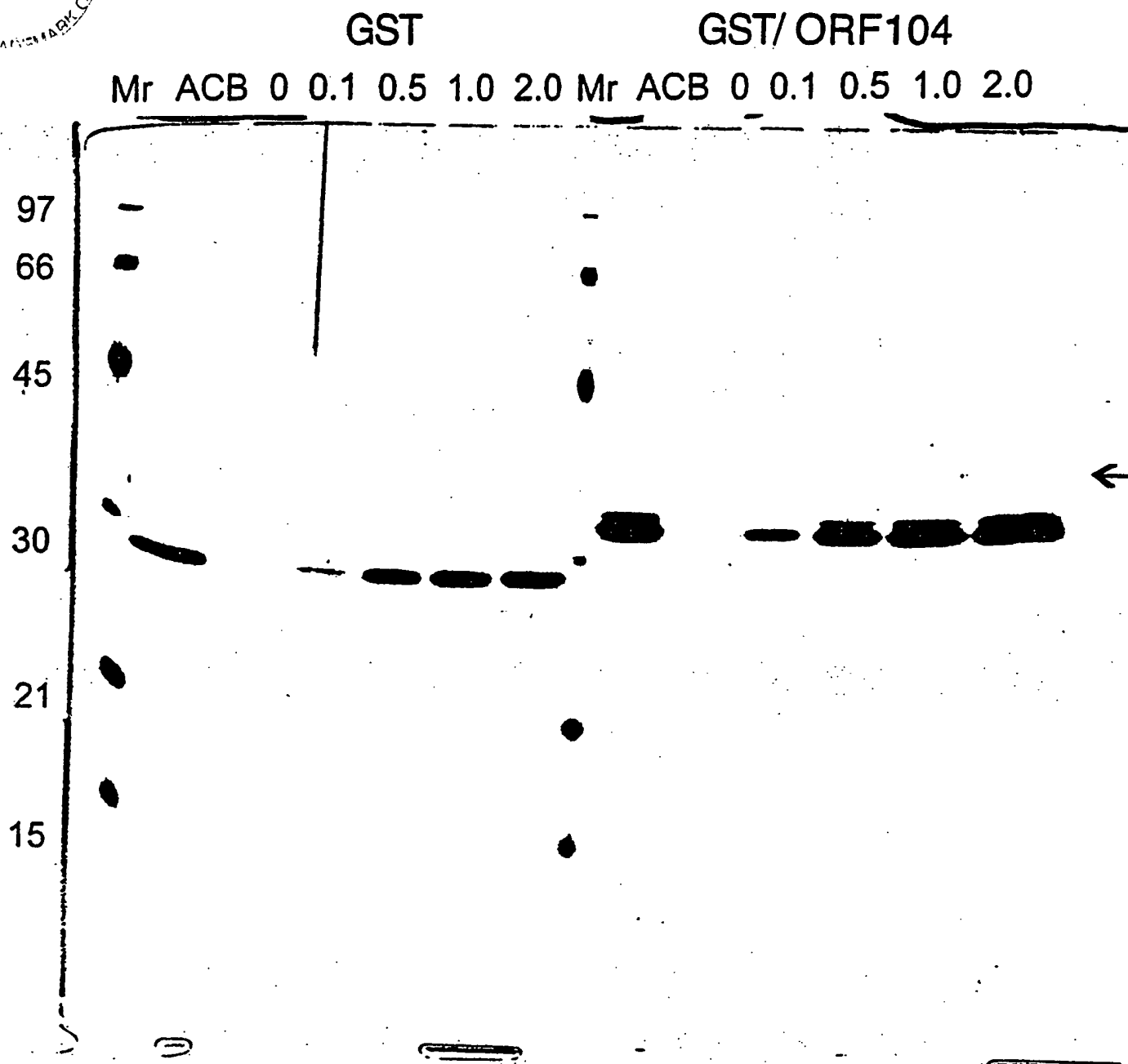
30

21

15



8C



SD



GST					GST/ ORF104					C	L			
ACB	0	0.1	0.5	1.0	2.0	Mr	ACB	0	0.1	0.5	1.0	2.0	2.0	2.0

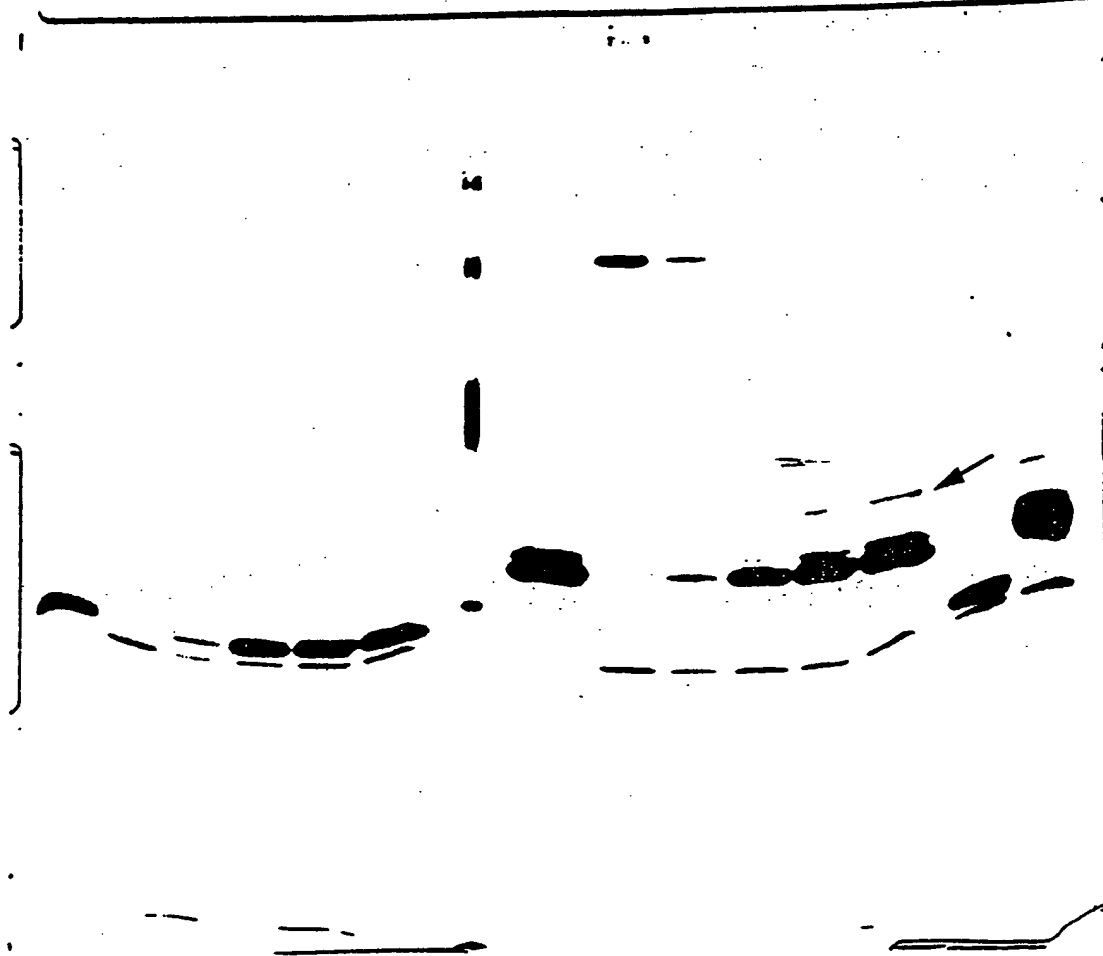
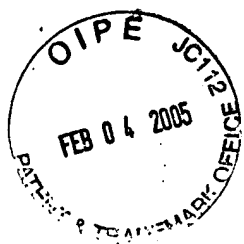


Fig. 9



Lys Extract FP/S Extract
ACB 0 0.1 0.5 1.0 2.0 Mr ACB 0 0.1 0.5 1.0 2.0

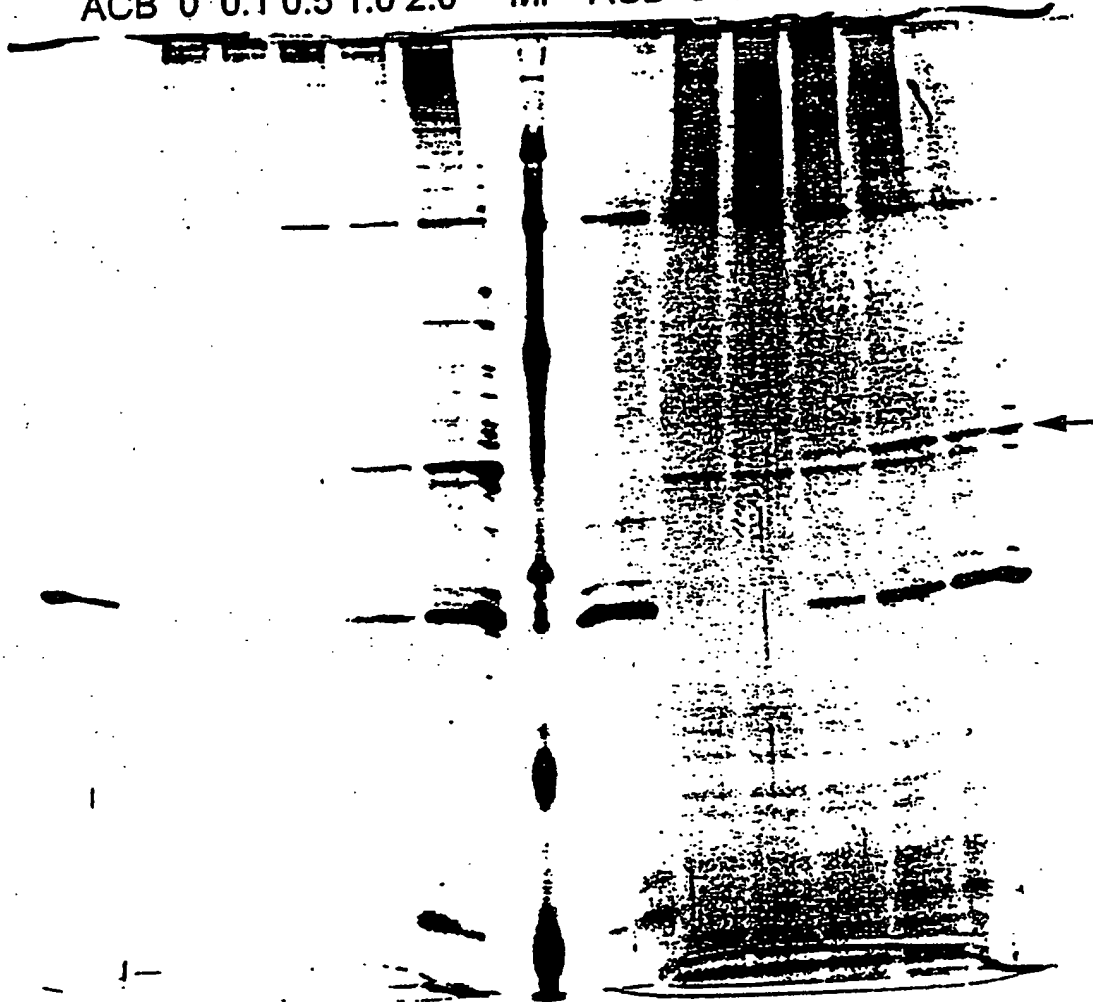


Fig. 10



Figure 11A:

i) Tryptic peptide mass spectrum of interacting protein (1% Triton X-100 elute)

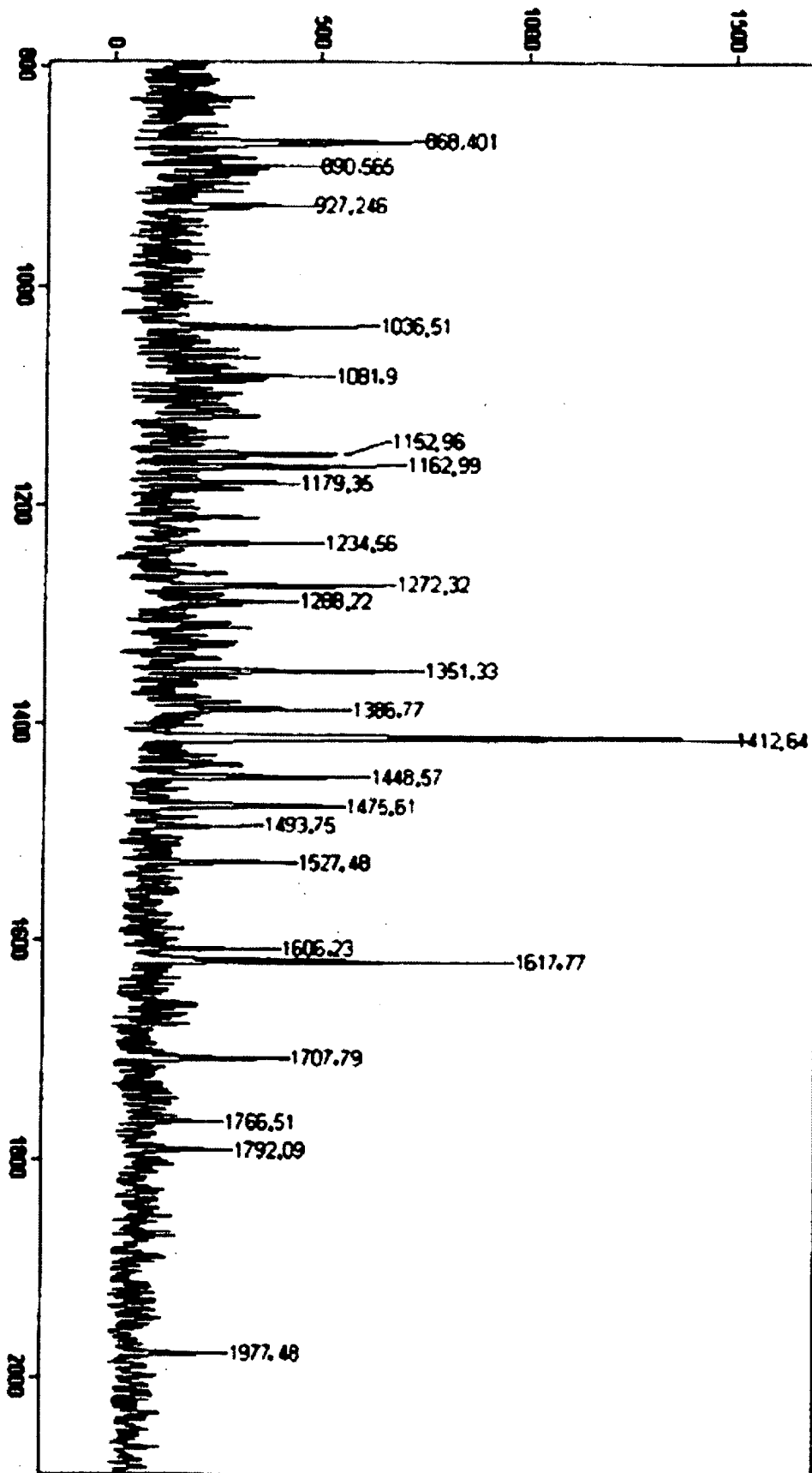




Figure 11B:
ii) Tryptic peptide mass spectrum of interacting protein (1% SDS eluate)

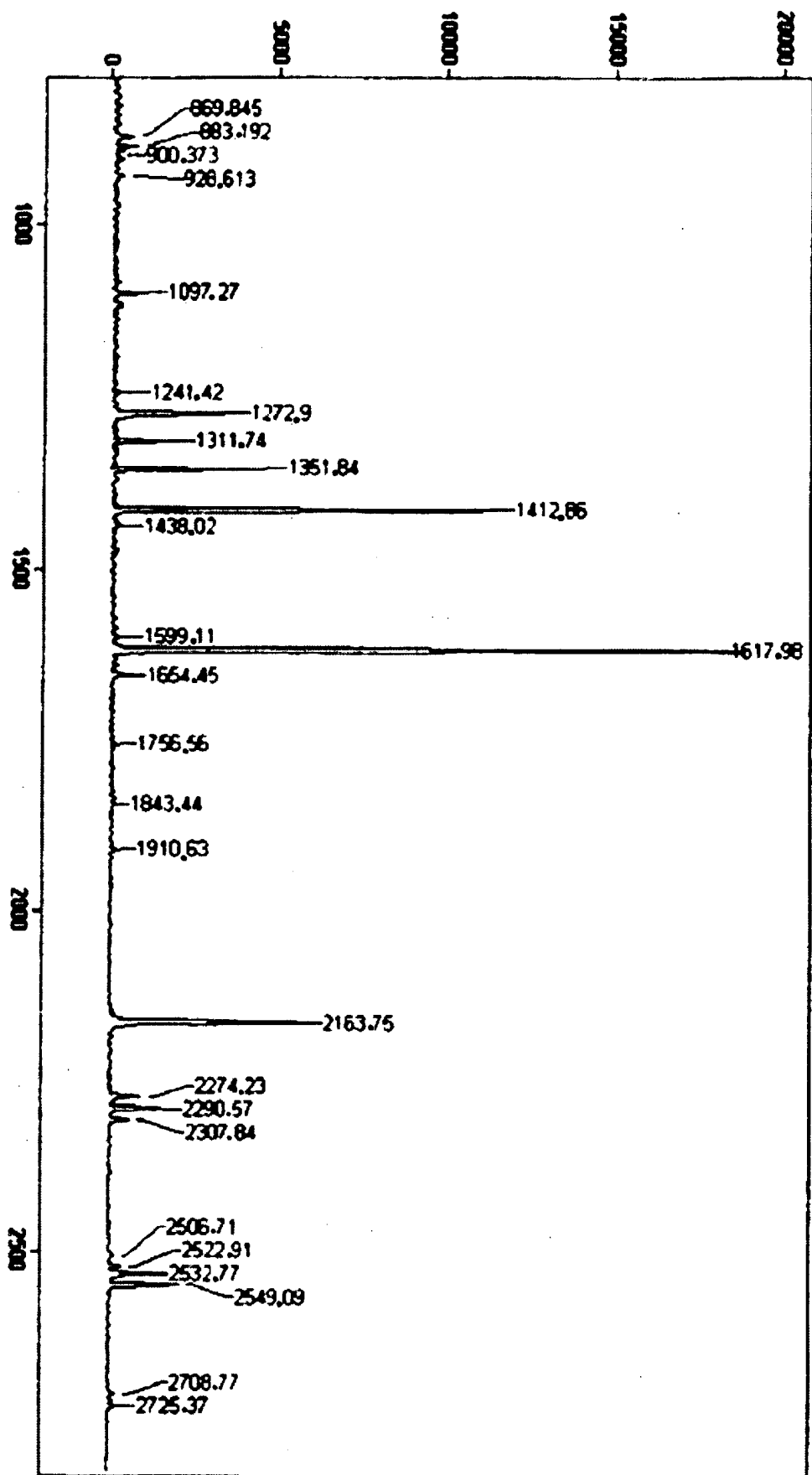
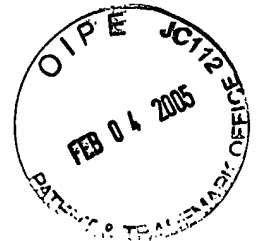
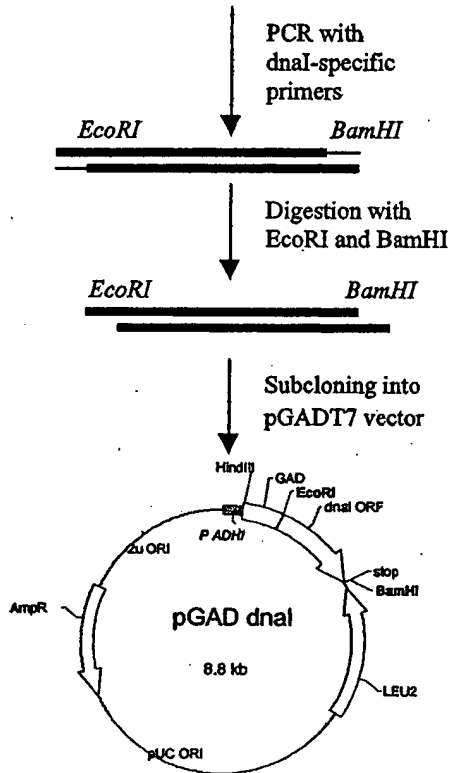


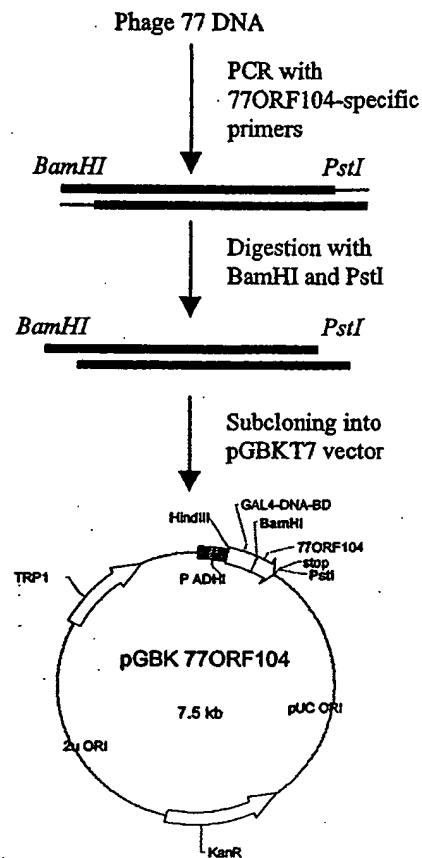
Figure 12



A- *Staphylococcus aureus* genomic DNA



B-



C-

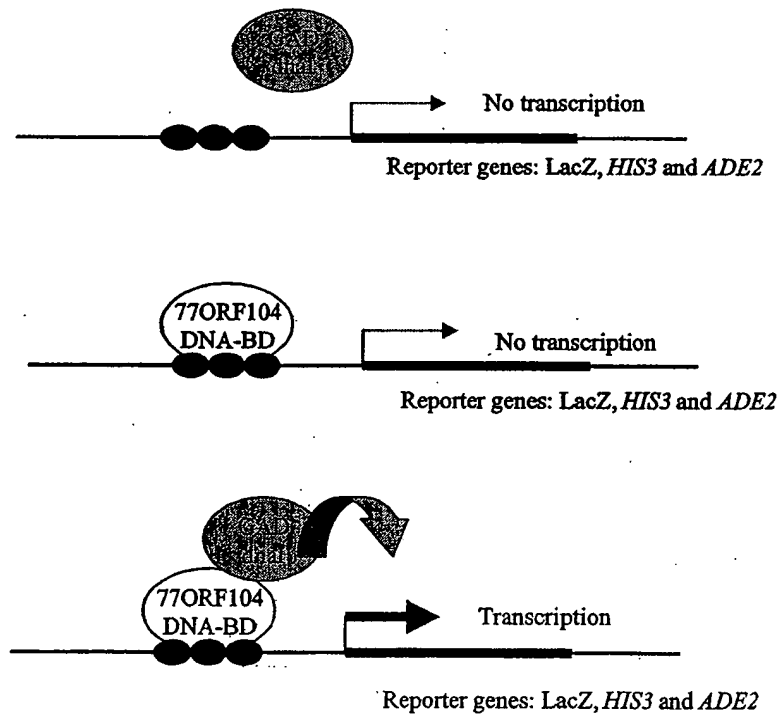
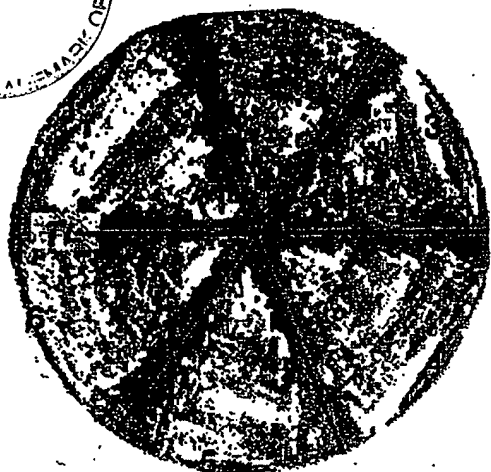
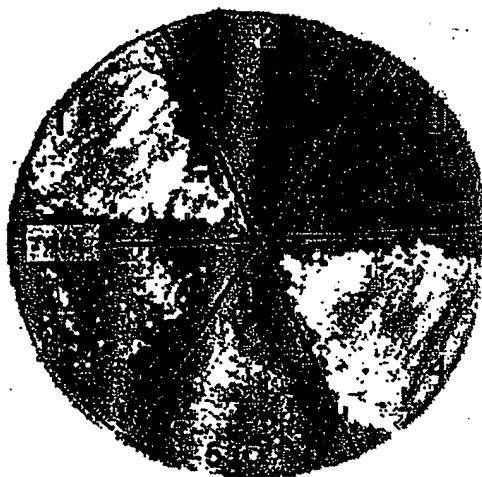




Fig 12 D+E



SD plate without Trp and Leu



SD plate without Trp, Leu, His and Ade

- 1) pGBKT7-53 and pGADT7-T
- 2) pGBKT7-53 and pGAD dna I
- 3) pGBK77ORF104 and pGADT7-T
- 4) pGBKT7-LAM and pCL1
- 5) pGBK77ORF104 and pGAD dna I
- 6) pGBK dna I and pGAD77ORF104

E)

Luminescent 5-Galactosidase Assay

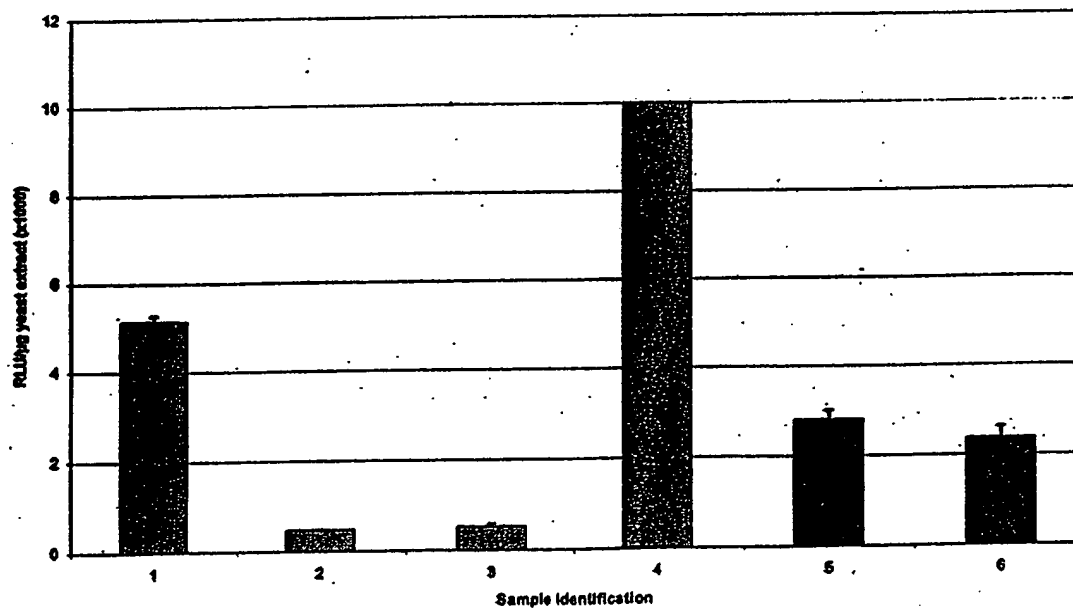
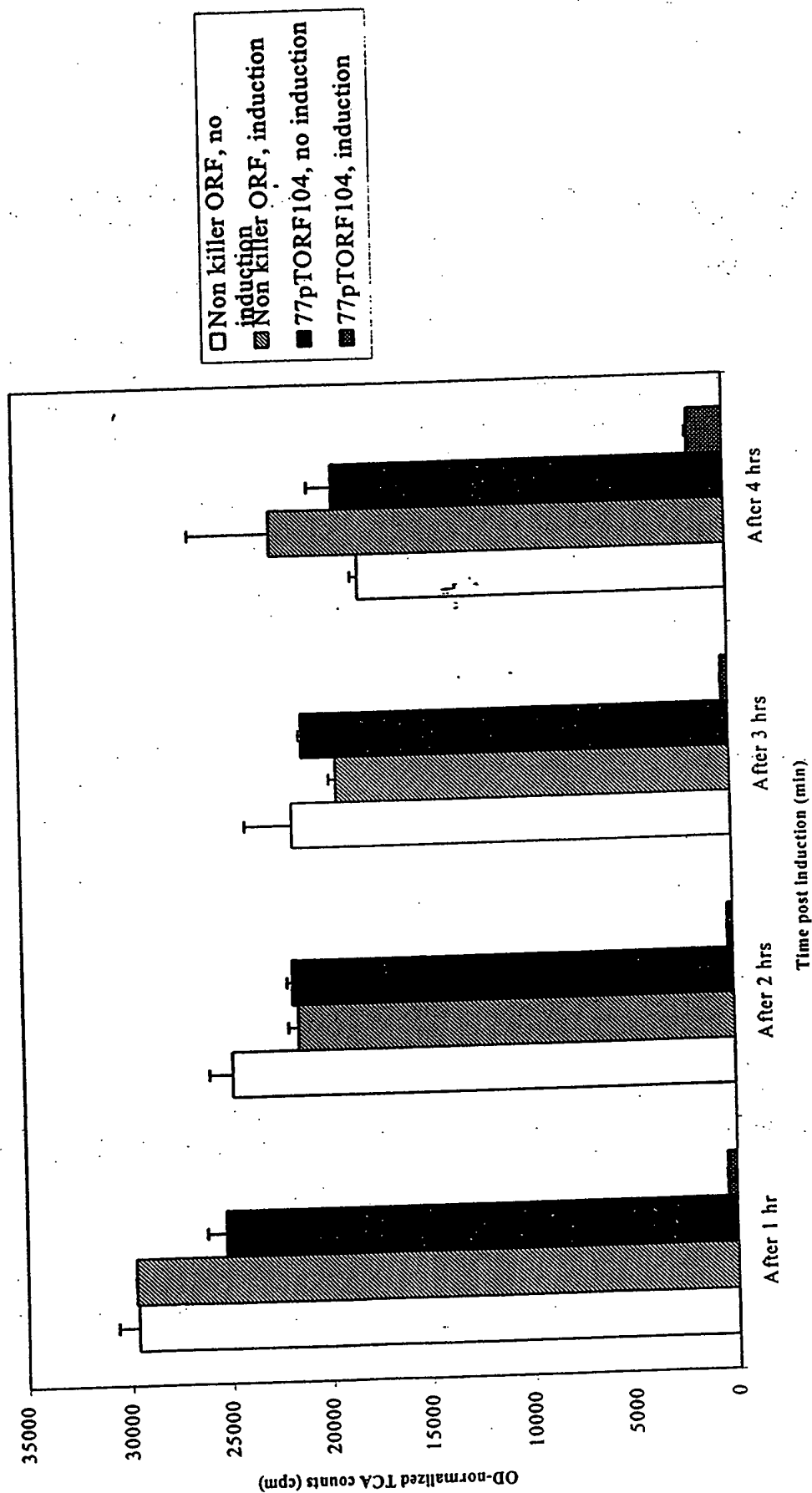


Fig. 13

Effect of 77ORF 104 expression on 3H-Thymidine incorporation



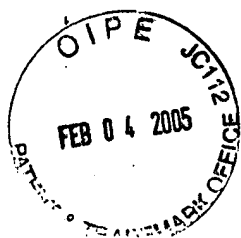
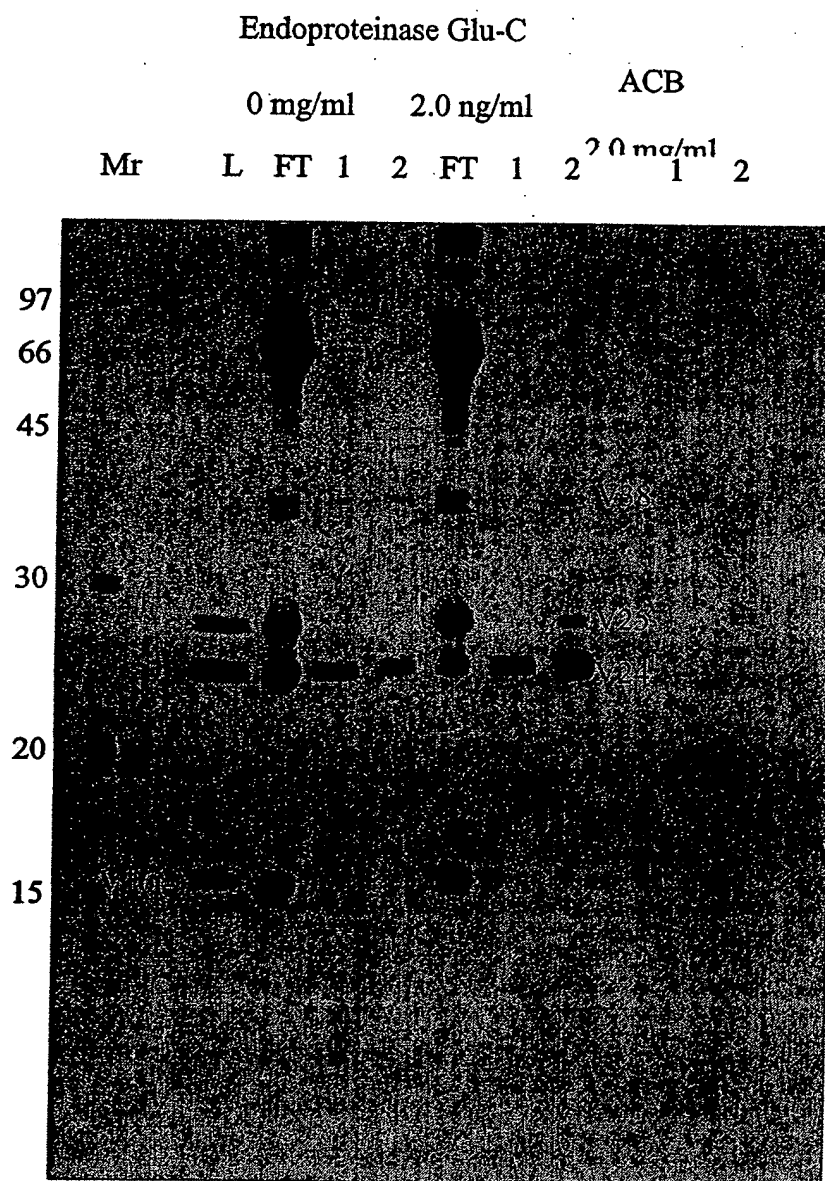


FIGURE 14A



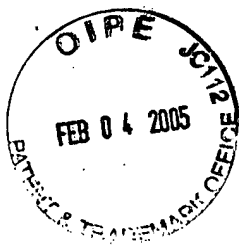


FIGURE 14B

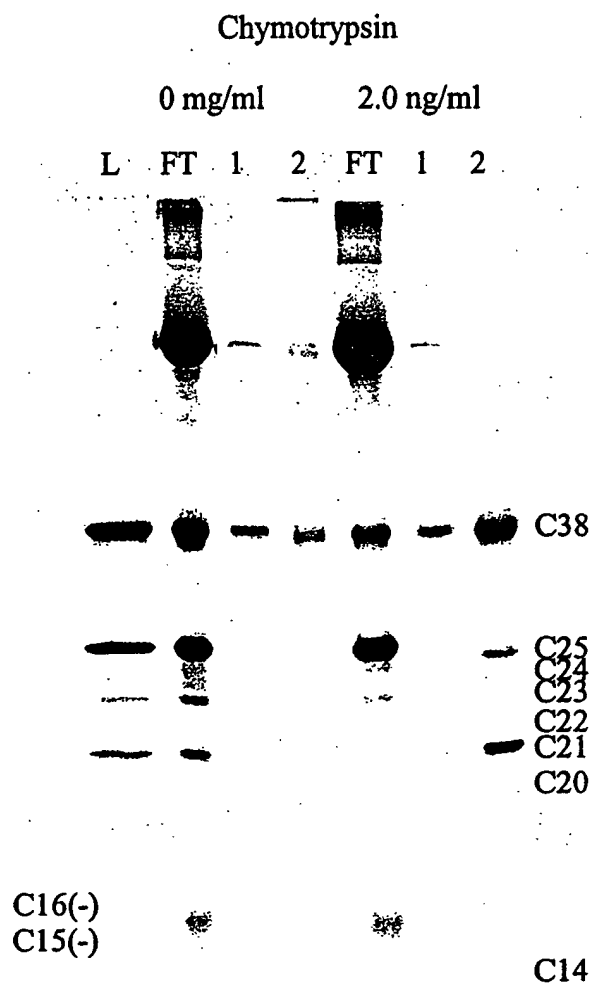




FIGURE 14C

Amino acid residues corresponding to interacting partial proteolytic fragments.

Protease	Proteolytic fragment ID (from Fig. 14A, B)	ID of SEQ ID NO: 2 fragment interacting with 77ORF104	
		from amino	to carboxyl
Endoproteinase Glu-C	V24	117	313
	V24	119	313
Chymotrypsin	C38	12	313
	C25	83	313
	C24	77	305
	C23	77	304
	C22	116	313
	C21	131	313
SEQ ID NO: 2	Complete	1	313



FIGURE 15

SEQ ID NO: 16

>*S.aureus* dnaI : amino acid 150-313

AADDICTAITNGEQVKGLYLYGPFGTGKSFILGAIANQLKSKKVRSTIIYLPEFIRTLKG
GFKDGSFEKKLHRVREANIIMLDDIGAEVTPWVRDEVIGPLLHYRMVHELPTFFSSNFD
YSELEHHLAMTRDGEKTKAARIIERVKSLSTPYFLSGENFRNN

SEQ ID NO: 17

>*S.aureus* dnaI : nucleotide 448-942

gcagcagatgatatttgtagcaataactaatggggaacaagtgaaggcctttacctt
tatggtccatttgggacaggtaaatcttttattctaggtgcaattgcgaatcagctcaa
tctaagaaggtagcttcgacaattatttattaccggaatttattagaacattaaaaggt
ggctttaagatggttcttttgaaaagaaattacatcgcgtaagagaagcaaacatttta
atgcttgatgatattggggctgaagaagtgactccatgggtgagagatgaggaattgga
cctttgctacattatcgaaatggttcatgaattaccaacattctttagttctaattttgac
tatagtgaattggaacatcatttagcgatgactcgtgatggtgaagagaagactaaagca
gcacgtattattgaacgtgtcaaactctttgtcaacaccatactttttatcaggagaaaat
ttcagaaacaattga

SEQ ID NO: 18

>*S.aureus* dnaI : amino acid 64-313

YKDQOKHYDGHKFADCPNFVKGHVPELYVDNNRIKIRYLQCPCKIKYDEERFEAELITSHH
MQRDTLNAKLKDIYMNHRDLVDMAADDICTAITNGEQVKGLYLYGPFGTGKSFILGAI
ANQLKSKKVRSTIIYLPEFIRTLKGGFKDGSFEKKLHRVREANIIMLDDIGAEVTPWVR
DEVIGPLLHYRMVHELPTFFSSNFDYSELEHHLAMTRDGEKTKAARIIERVKSLSTPYF
LSGENFRNN

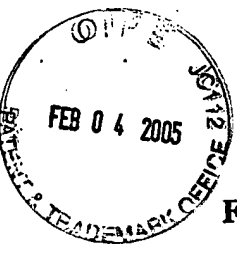
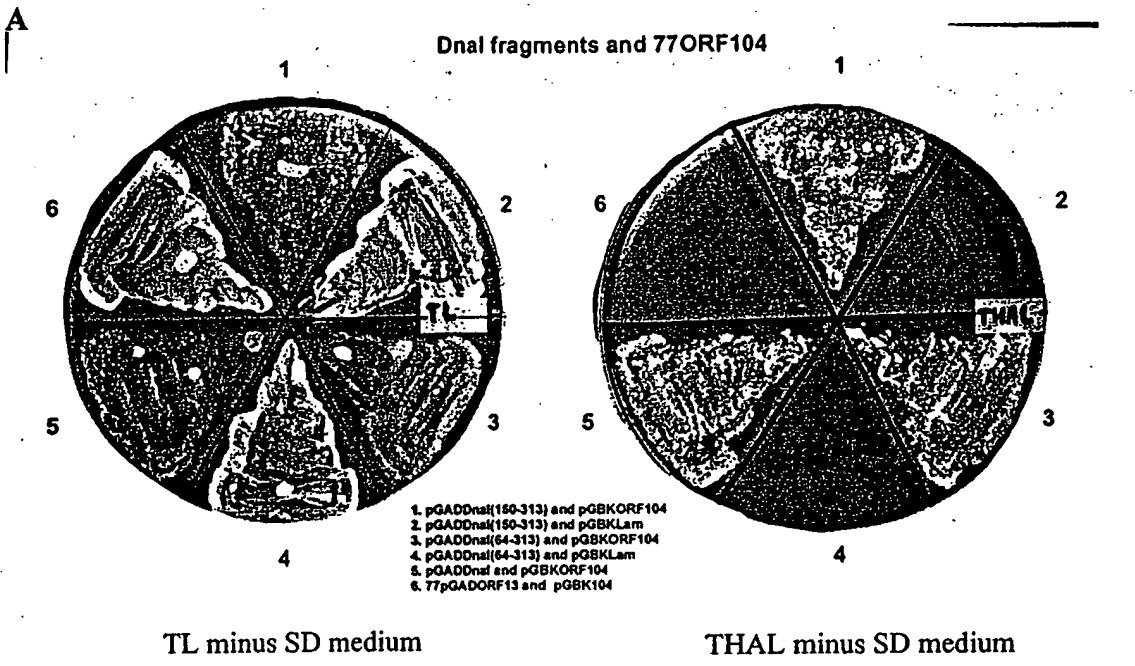


FIGURE 16



B

			Interaction with 77 ORF 104
SEQ ID NO: 2		313	yes
SEQ ID NO: 18	64	313	yes
SEQ ID NO: 16	150	313	yes

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